

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_Plus\_p2n model

Run on: November 23, 2003, 11:53:01 ; Search time: 354 seconds

(without alignments)

2437.305 Million cell updates/sec

Title: US-10-045-594D-2

Perfect score: 1

Sequence: MLSHTMMKORKQOATAIMK.....PIVITTEPTDDTTVPESEDL 264

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5

Ygapop 10.0 Ygapext 0.5

Fgapop 6.0 Fgapext 7.0

Delop 6.0 Delexc 7.0

Searched:

2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters:

4339922

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line Parameters:

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-Q=/cgn2_1/USP01.spoof/US1045594/runat_21112003_162202_17166/app/query.fasta_1.455
-DB=published Applications NA -QFORMAT=astar -PREFIX=p2n_rnpb -MINMATCH=0.1
-LOOPCL=0 -LOCPEXT=0 -INITS-bits -START=1 -END=1 MATRIX=blosum62
-TRANS-human40-cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFILEPCTO -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=000000000 -USER=US10045594 @cgn_1_1_247 @runat_21112003_162202_17166
-NCPOL=6 -ICPOL=6 -NO_MMAP -LARGEQUERY -NEG -DSPBLOCK=100
-LONGL -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Published Applications NA.\*

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Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

ALIGMENTS

RESULT 1

; Sequence 286, Application US/10098841

; GENERAL INFORMATION:

; Publication No. US20030197679A1

; Sequence 129, Application US/10-311-055-1219

; Sequence 1, Application US/10-156-761-1

; Sequence 53, Application US/09-771-161A-53

; Sequence 73, Application US/10-354-587-73

; Sequence 366, Application US/10-311-081-366

; Sequence 1913, Application US/10-311-055-1913

; Sequence 203, Application US/10-240-153-203

; Sequence 179, Application US/10-239-676-179

; Sequence 19824, Application US/09-814-553-18824

; Sequence 13, Application US/09-816-669A-13

SUMMARIES

Result Query Match Length DB ID Description

No. Score

1 1395 100.0 1119 13 US-10-098-841-286 Sequence 286, App

TITLE OF INVENTION: No. US20020197679A1 Nucleic Acids and Polypeptides

FILE REFERENCE: 784CIP2

CURRENT APPLICATION NUMBER: US/10/098-841

CURRENT FILING DATE: 2002-03-13  
; PRIORITY APPLICATION NUMBER: 09/598,042 not pb  
; PRIORITY FILING DATE: 2000-06-20  
; PRIORITY APPLICATION NUMBER: 09/552,317 not pb  
; PRIORITY FILING DATE: 2000-04-15  
; PRIORITY APPLICATION NUMBER: 09/488,725 not pb  
; PRIORITY FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 331  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO: 286  
; LENGTH: 1119  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (128)..(922)  
; US-10-098-841-108

Alignment Scores:

Pred. No.	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:
5_39e-155	1119	135.00	100.00%	100.00%	100.00%
	Matches: 264	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 13

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Cy 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys  
Db 128 ATGCTATACATAATACTATGATGAGCAGAAACAGAACAGCAATATGAG

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 188 GAGTCATGGAAATGATGTTGATGGATGACCTGGCAAAGAACTGACATCCCGAGA 247

QY 41 AspIleMetLeuGluGluLeuSerHisLeuSerAsnArgGlyAlaArgLeuPheLysMet 60  
Db 248 GAGATCATGTTGGAGRATTATGCCATCTCATGTTACCGTGTGCCAGGGCTATTAAAGTG 307

QY 61 ArgClnIargGserAspLystyrThnPheGluAspPheGlnTrpGlnSerGalaGin 80  
Db 308 CGTCAAAGAAGATCTGACAAAATCACATTGAAATTCCAGTACAATCTAGGCACAA 367

QY 81 IleAsnHisSerIleAlaMetGlnAsnGlyIysValAspGlySerAsnLeuGluGly 100  
Db 368 ATAATATCAGTGTGCTATGAGTAATGGGGAAATGTGGATGAACTCTCTGAAATTCAAC 427

QY 101 SerGlnGlnIaproLeuThrProAspProSerProAsnPro 120  
Db 428 TCCAGCTTAAAGCCCCCTTCACTTCCAAACCCCAGTCACGAGCCCTCAAAATCC 487

QY 121 AspAsnIleAlaProGlyTyrSerGlyProLeuLysGluLeuSerAsnLeuGluGly 140  
Db 488 GAAZACATGCTCAGATATTGACCATTGAAATTCCTCTGAAATTCAAC 547

2Y 141 ThrThrAlaValProLysTyrGlnSerProTrpGluGlnAlaIleSerAsnAsnPro 160  
Db 548 AACACAGTGTGCTTAAGTCAATGACTCAAACTCTCTGGAAACAGGATTGAAATGGCT 607

2Y 161 GluLeuLeuGluIleUtyProLysLeuPheLysProGluGlyLysAlaGlnLeuPro 180  
Db 608 GAGCTTTPAGAGCTTATACTTCAAACTTCAAGCTGAGGAAGGAGAACCTGCT 667

2Y 181 AspTyrArgSerPheAsnArgValAlaThrProPheGlyGlyPheGluLysAlaSerArg 200  
Db 668 GATTACAGGAGCTTAAACAGGTTGCAACACATTGGAGGTTTGAAAGGCCTCAACAA 727

2b 201 MetValLysPheLysValProAspPheGluLeuLeuIeuAspProArgIleMet 220  
Db 728 ATGGTTAAATTAAAGTTCAAGATTGAGCTACTATGCTAACAGATCCAGTTATG 787

221 SerpheValAsnProLeuSerGlyArgArgSerPheAsnArgThr-ProLysGlyTrpIle 240

Db 788 TCCCTTGTCATAATCCCTTTCCTGGCAGAGGTTTTAATGGACTCTTAAGGATGATA 847  
Qy 241 SerGluAsnIleProLeuValIleThrThrGluProThrAspAspThrValProGlu 260  
Db 848 TCTGAGAAATATCTTATAGTGTAAACACGAACTACAGTGTACACACTTACACGAA 907

Qy 261 SerGluAspIle 264  
Db 908 TCAGAGAACCTA 919

RESULT 2  
US-09-918-995-3415  
; Sequence 3415, Application US/0918995  
; Publication No. US200301073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIORITY APPLICATION NUMBER: US/09/235,076  
; PRIORITY FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 3415  
; LENGTH: 434  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-3415

Alignment Scores:

Pred. No.	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:
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US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
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DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
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QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIleSerIleAsnThrMetMetLeuSerGlnArgLysGinGlnAlaThrAlaIleMetLys 20  
Db 124 ATGCTATACATAATACTATGATGTTGAAATTCATCCATGCTGAGCAACAGCTCATGAG 183

QY 21 GluValHisGlyAsnAspVaAspGlyMetAspLeuGlyLysLeuSerIleProArg 40  
Db 184 GAAGTCATGAAATGATGTTGATGCTGAGCTGAGTGGCAAAAGGTCAAGCTCCCGAGA 143

DB: 11

US-10-045-594D-2 (1-264) x US-C9-918-995-3415 (1-434)

QY 1 MetIle